REMARKS

Amendments

Support for the amendments to claim 1 is found in canceled claim 2 and in the specification at, for example, page 2, lines 16-18. Support for the amendment to claim 8 is found at page 24, lines 13-22. No new matter is introduced by these amendments.

A "marked up" version of the claims showing the changes made and an appendix of the claims as pending are attached.

The Office Action

An objection is raised to the title, abstract, and presence of browser-executable code in the specification. An objection is also raised against claim 9 as a duplicate of claim 2.

Claims 1-13 and 15-26 are pending in this application. Claim 12 is rejected under 35 U.S.C. § 101. Claims 1-13 and 15-26 stand rejected under 35 U.S.C. § 112, first paragraph. Claims 1-13 and 15-26 stand rejected under 35 U.S.C. § 112, second paragraph. Claims 1-13, 15-19, and 21-26 are rejected under 35 U.S.C. § § 102(a) and (b). Claims 1-13, 15-19, and 21-26 stand rejected under 35 U.S.C. § 103(a). Each of these objections and rejections is addressed as follows.

Specification and Claim Objections

Applicants note that the title of the invention and the abstract of the disclosure are amended to be descriptive of the invention as claimed.

Applicants are unable to identify any browser-executable code in the specification. Accordingly, no amendments are made.

Claim 2 is canceled herewith and its limitations incorporated into claim 1. Claim 9 is amended to depend from claim 8.

In view of the aforementioned amendments and comments, applicants request that the objections to the specification be withdrawn.

A "marked-up" version of the title and abstract showing the changes made is attached.

Rejections Under 35 U.S.C. § 101

Claim 12 stands rejected under 35 U.S.C. § 101 for encompassing non-statutory subject matter. Specifically, the Examiner notes that claim 12 reads on a product of nature. In response, applicants have amended the claim according to the Examiner's suggestion and this rejection may now be withdrawn.

Rejections Under 35 U.S.C. § 112, first paragraph

Claims 1-13 and 15-26 stand rejected under 35 U.S.C. § 112, first paragraph, for both lack of enablement and an inadequate written description.

Scope of Enablement

Claims 1-13 and 15-22 stand rejected under § 112, first paragraph based on the assertion that the teaching of applicants' specification is not commensurate in scope with the present claims. The rejection essentially turns on the assertion that it would require undue trial and error experimentation to identify genes having at least 30% identity to the disclosed *Arabidopsis* SSE polypeptide (SEQ ID NO:2). This rejection should be withdrawn.

Applicants first point out that the Federal Circuit has made clear the level of teaching needed to enable a claim, and has repeatedly stated that a patent need not reiterate techniques known to skilled workers in a particular area of technology. *See Hybritech Inc. v. Monoclonal Antibodies, Inc.*, 802 F.2d 1367, 231 U.S.P.Q. 81 (Fed. Cir. 1986), *cert. denied*, 480 U.S. 947 (1987); *In re Wands*, 858 F.2d 731, 8 U.S.P.Q.2d 1400 (Fed. Cir. 1988); *Spectra-Physics, Inc. v. Coherent, Inc.*, 827 F.2d 1524, 3 U.S.P.Q.2d 1737 (Fed. Cir. 1987), *cert. denied*, 484 U.S. 954 (1987) ("A patent need not teach, and preferably omits, what is well known in the art."); *see also Paperless Accounting, Inc. v. Bay Area Rapid Transit Sys.*, 804 F.2d 659, 231 U.S.P.Q. 649 (Fed. Cir. 1986) ("A patent

applicant need not include in the specification that which is already known to and available to the public.").

In view of this standard, applicants submit that their specification clearly enables the subject matter presently claimed. In particular, given the teaching of the specification and the level of skill known in the art at the time the present application was filed, applicants submit that plant genes encoding SSE polypeptides falling within the scope of applicants' claims could be routinely identified and isolated from plants other than *Arabidopsis*, and utilized, as outlined in applicants' specification, by employing standard techniques of molecular biology.

The Examiner has the initial burden to establish a reasonable basis to question enablement. In *In re Marzocchi*, 439 F.2d 220, 169 U.S.P.Q. 367, 369 (CCPA 1971), the court stated:

> a specification disclosure which contains a teaching of the manner and process of making and using the invention in terms which correspond in scope to those used in describing and defining the subject matter sought to be patented must be taken as in compliance with the enabling requirement of the first paragraph of § 112 unless there is reason to doubt the objective truth of the statements contained therein which must be relied on for enabling support.

The MPEP (§ 2164.04) echoes the findings of *Marzocchi*:

> (I)t is incumbent upon the Patent Office, whenever a rejection on this basis is made, to explain why it doubts the truth or accuracy of any statement in a supporting disclosure and to back up assertions of its own with acceptable evidence or reasoning which is inconsistent with the contested statement. Otherwise there would be no need for the Appellant to go to the trouble and expense of supporting his presumptively accurate disclosure.

In an attempt to cast doubt on the enablement aspects provided in the instant specification, the Examiner cites several references that purportedly provide evidence that predicting the function of an altered protein is an inherently difficult proposition.

According to the Examiner, the collective teachings of Bowie *et al.* (Science 247:1306-1310, 1990), Lazar *et al.* (Mol. Cell. Biol. 8:1247-1252, 1988), Broun *et al.* (Science 282:1315-1317, 1998), and Hill *et al.* (Biochem. Biophys. Res. Comm. 244:573-577, 1998) tend to show that even small changes in the primary amino acid sequence of a protein can result in unpredictable alterations in function.

The Examiner's reliance on these references is misplaced. To the extent that the Examiner suggests, not every SSE peptide would be successfully identified, this does not mean the present claims are overbroad. The Federal Circuit has long held that it is not necessary for all possible embodiments of a claim to be operative in order for that claim to be enabled. *See Atlas Powder Co. v. E.I. du Pont de Nemours & Co.*, 750 F.2d 1569, 224 U.S.P.Q. 409 (Fed. Cir. 1984). The proper test of enablement is "whether one reasonably skilled in the art could make or use the invention from the disclosures in the patent coupled with the information known in the art without undue experimentation." *Hybritech, Inc. v. Monoclonal Antibodies, Inc.* 802 F.2d. 1318 (Fed. Cir. 1985). In analyzing what constitutes undue experimentation, the MPEP (§ 2164.06) cites *In re Wands*, (858 F.2d 731, 8 USPQ2d 1400 (Fed Cir. 1988)):

> The test is not merely quantitative, since a considerable amount of experimentation is permissible, if it is merely routine, or if the specification in question provides a reasonable amount of guidance with respect to the direction in which the experimentation should proceed. (Emphasis added.)

At the time of filing, a skilled artisan, using no more than routine experimentation and the teachings of the present specification, could easily screen genes for identifying SSE polypeptides. Such screening could easily be accomplished using standard techniques for generating and screening recombinant gene libraries and thus does not constitute undue experimentation. The present situation is, in all important aspects, indistinguishable from the facts in *Wands* in which the Federal Circuit held that the applicant's claim was enabled, despite the necessity for screening, because the process of screening was straightforward. It follows that the present claims are also enabled, even if some screening would be necessary to identify additional genes encoding functional SSE

polypeptides. As such, applicants have already demonstrated the feasibility of their invention by a successful working example, using routine methods.

In addition, on gene isolation, applicants point out that clear instructions for isolating additional SSE cDNA gene sequences are provided in their specification at pages 22-25. There, under the heading "Isolation of Other SSE Genes," applicants provide general guidance on the routine methods known at the time the application was filed for identifying and characterizing the gene sequences required by the claims. These standard methods described in the specification include: (1) the design and utilization of oligonucleotides for cloning SSE gene sequences, (2) hybridization cloning methodologies, (3) library screening procedures, (4) PCR-based amplification cloning strategies, and (5) cDNA expression library cloning techniques. These methods, alone or in combination, are effective for isolating and cloning desired SSE gene-specific products.

Once isolated, these genes are used directly to modulate SSE activity in a plant, exactly as described by applicants, for example, at pages 38-41 of the present specification. Moreover, once candidate plant gene sequences encoding SSE polypeptides are isolated, standard DNA sequencing may also be used to confirm their relatedness to known sequences. Publicly available sequence analysis software allows for the rapid identification of proteins encoded by such sequences falling within the scope of applicants' claims.

Furthermore, once a candidate sequence is created or identified, the specification provides several screening assays to determine whether such polypeptide functions as an SSE polypeptide as presently claimed. For example, an SSE polypeptide should be able to complement the "shrunken seed" phenotype, described on page 16, when transfected into an *Arabidopsis sse1* mutant. The results for SEQ ID NO:2, for example, presented in Figure 4B demonstrate such phenotypic reversal. The seeds obtained from *sse1* plants expressing an SSE1 transgene have lost the shrunken seed appearance and are phenotypically identical to wildtype seeds (compare with Figure 1E and 1F).

In addition, applicants' specification teaches still another functional screen which enables the artisan to determine whether a candidate protein is, in fact, an SSE polypeptide falling within the scope of the claims. For example, candidate SSE genes may be tested for the ability to complement a yeast *pex16* mutant as described at page 19, line 20, through page 21, line 9.

Each of the methods described for isolating and characterizing the claimed gene sequences involves standard techniques routinely used in the art of molecular biology at the time applicants filed their application. It is improper to find that such experimentation is "undue" simply because it requires some "trial and error," *W.L. Gore & Assoc. V. Garlock, Inc.* 721 F.2d 1540, 1557, 220 U.S.P.Q. 303, 316 (Fed. Cir. 1983), even when the experimentation is needed to weed out inoperative embodiments. *Atlas Powder v. E.I. DuPont deNemours*, 750 F.2d 1569, 1576-77, 224 U.S.P.Q. 409, 414 (Fed. Cir. 1984).

Turning to claims 23-26, which are generally directed to vectors including SSE antisense RNAs and plants including such vectors, applicants' point out that the scientific reality is that antisense technology works. There was no debate in the scientific community that antisense regulation of gene expression was an acceptable, if not universal, method for gene regulation in plants when applicants filed their provisional patent application in 1999. In 1992, the Patent Office acknowledged this when it issued U.S. Pat. No. 5,107,065, titled "Antisense Regulation of Gene Expression in Plant Cells" to Calgene. Calgene was awarded its patent for work on the Flavr-Savr Tomato, a tomato that uses antisense technology to inhibit the polygalacturonase, an enzymatic component in the softening of the tomato.

All of the tools for antisense expression of a SSE gene in a plant were known when applicants filed their patent application: vectors containing promoters and terminators. Indeed, exemplary expression vectors, promoters, and terminators are described in the specification, for example, at pages 31-32. Moreover, applicants in their specification, for example, at pages 34-38 describe several methods for introducing the vectors into host cells such as plant cells, and regenerating transformed plants. Plants

expressing antisense RNA are then selected by visual examination (as described, for example, in Figure 4B) or by using standard techniques for RNA analysis (as described, for example, at page 10 (ll. 23) through page 11 (ll.11)).

To support this ground of rejection, the Examiner cites several scientific publications to demonstrate that the use of antisense nucleic acids for reducing gene expression is inherently unpredictable. But, rather than proving "unpredictability" in the art of antisense regulation of gene expression, the publications cited by the Examiner evidence the routine nature of making and screening large numbers of transformants to identify plants with altered characteristics. In particular, as noted by the Examiner, the majority of the references -- van der Krol, Bird, Kuipers, Klann, and Tang – provide results for successfully reducing gene expression by transforming plants with vectors encoding antisense RNAs. Indeed, inhibition of expression was achieved for a variety of genes in different plant species.

Again, a specification cannot be found as failing to enable the claimed invention when the techniques required to practice the invention are disclosed in the specification and available to those skilled in the art. See *In re Wands, 858 F.2d* 731, 740, 8 USPQ2d 1400, 1406; *In re Strahilevitz*, 668 F.2d 1229,1232, 212 U.S.P.Q. 561, 563 (C.C.P.A. 1982). In short, no scientific hurdle and, consequently, no undue experimentation to antisense expression of an SSE RNA in plants has been demonstrated. Case-by-case experimentation is expected by researchers in the biotechnological arts and is not undue. See *Johns Hopkins University v. Cell Pro, Inc.*, 152 F.3d 1342, 1360, 47 U.S.P.Q.2d 1705, 1718-19 (Fed. Cir. 1998); *In re Wands*, 858 F.2d 731, 740, 8 U.S.P.Q.2d 1400,1406-07 (Fed. Cir. 1988). This case is therefore distinguishable from those cases where scientific hurdles blocked the practicing of the claimed invention. For example, the patent applicant in *In re Goodman* admitted that there was a specific "major block" to practicing the claimed invention, i.e., expressing mammalian proteins in monocots. *In re Goodman*, 11 F.3d 1046,1051, 29 U.S.P.Q.2d 2010, 2014 (Fed. Cir. 1993). ("Goodman's own 1987 article .... underscores the "major block" to using the claimed method in

monocot plant cells.") No such hurdle or block has been shown to exist in this case, and this basis of the enablement rejection should be withdrawn.

Written Description

Claims 1-13 and 15-26 stand rejected, under 35 U.S.C. § 112, first paragraph, as containing subject matter that was not described in the specification in such a way as to convey to one skilled in the art that the inventors had possession of the claimed invention. Applicants respectfully traverse this basis of the rejection.

To provide a description of an invention, applicants in their specification need only 'convey clearly to those skilled in the art to whom it is addressed...the information that [the inventor] has invented the specific subject matter later claimed.'" *Martin v. Mayer*, 823 F.2d 500, 505, 3 U.S.P.Q.2d 1333, 1337 (Fed. Cir. 1987). Applicants submit that they have satisfied this standard.

The claimed invention encompasses DNA molecules encoding a polypeptide having at least 30% identity to SEQ ID NO:2 or hybridizing under low stringency conditions to SEQ ID NO:1, and having the biological activity of the SSE polypeptide. In addition, applicants' specification specifically describes at least two structural features of the claimed sequences: hydrophobic and hydrophilic domains as described in, for example, Fig. 2B. Further, applicants' specification describes the requisite biological activity of an SSE polypeptide. According to applicants' specification, an SSE polypeptide complements the shrunken seed phenotype when introduced into a n sse1 mutant (see, for example, page 16 (ll. 12) through page 12, line 22)) or the pex16 mutation in Y. lipolytica (see, for example, page 19 (ll. 20) through page 21 (ll. 9)). Such a description readily enables the skilled worker to identify plant SSE polypeptides falling within the claimed subject matter, and therefore satisfies the written description requirement of § 112. This rejection may be withdrawn

Rejections Under 35 U.S.C. § 112, second paragraph

Claims 1-13 and 15-26 stand rejected under 35 U.S.C. § 112, second paragraph, for indefiniteness. Each of the Examiner's rejections is addressed below.

The Examiner asserts that the abbreviation "SSE" is indefinite and rejects claims 1-13 and 23. Applicants respectfully disagree. The specification clearly teaches an SSE polypeptide as being encoded by a gene that, when inactivated, generates the so-called "shrunken seed" phenotype (see, for example, Figure 1, and page 16, line 12, through page 17, line 22). Furthermore, applicants identify the nucleotide and amino acid sequences of the *Arabidopsis* SSE1 in SEQ ID NOs: 1 and 2, respectively (page 18, lines 7-8). Claim 1 is also amended to require that SSE1 polypeptides of the present invention are at least 30% identical to SEQ ID NO: 2. Thus, when read in conjunction with the specification, the abbreviation "SSE" is clear and definite.

Claim 16 is amended in accordance with the Examiner's suggestions.

Claim 8 is amended to require hybridization under low stringency conditions. Appropriate conditions for low stringency hybridization are found in the specification at page 24, lines 13-22.

In view of the aforementioned amendments, applicants request reconsideration and withdrawal of the section 112, second paragraph rejections.

Rejections Under 35 U.S.C. § 102

Claims 12, 13, 16-19, and 21-22 stand rejected under 35 U.S.C. 102(b) as being anticipated by Akama *et al.* (Plant Cell Rep. 12:7-11, 1992). Claims 1, 7, and 11-12 stand rejected under 35 U.S.C. 102(b) as being anticipated by Mukai *et al.* (Gene 132:57-66, 1993). Claims 1-5, 7-9, and 11-12 stand rejected under 35 U.S.C. 102(b) as being anticipated by Storozhenko *et al.* (FEBS Lett. 390:113-118, 1996). Claims 1-12 stand rejected under 35 U.S.C. 102(a) as being anticipated by Rounsley *et al.* (GenBank Accession Nos: T00882 and F84893, February 1999). Claims 1, 3-6, 10-13, 15-18, and 21-26 stand rejected under 35 U.S.C. 102(a) as being anticipated by Leborgne-Castel *et al.* (Plant Cell 11: 459-469, 1999) in view of Galili *et al.* (Plant Mol. Biol. 35:1-29, 1998). Claims 1, 3-7, 10-13, 15-19, and 21-26 stand rejected under 35 U.S.C. 102(b) as being anticipated by Lee *et al.* (Mol. Gen. Genet. 252:11-19, 1996).

To anticipate a claim a prior art reference must disclose every limitation of the claims.

Claim 1, as amended, and its dependent claims, requires an isolated nucleic acid molecule that includes a sequence encoding an SSE polypeptide having at least 30% identity with the amino acid sequence shown in Fig. 2B (SEQ ID NO: 2). Because the Akama, Mukai, and Leborgne-Castel (in view of Galili and Lee) references do not teach this limitation, these references cannot anticipate claim 1.

In addition, for the following reasons, Storozhenko does not anticipate claims 1 and 8 (and claims dependent thereon). Claim 1 is discussed above. Claim 8, as amended, is limited an isolated nucleic acid molecule that hybridizes under low stringency conditions to a nucleic acid molecule that includes the cDNA of Fig. 2A (SEQ ID NO:1).

Storozhenko's HSP91 is identified as accession number Z70314 (see Figure 5 legend). An alignment of the HSP91 polypeptide and the SSE1 polypeptide (SEQ ID NO: 2) shows that these proteins do not share significant identity, much less 30% identity as required by claim 1. In addition, given the lack of identity at the amino acid level, it is unreasonable to assume that the gene encoding HSP91 has enough identity to hybridize under low stringency conditions to a nucleic acid sequence including SEQ ID NO:1, which encodes the *Arabidopsis* SSE polypeptide (SEQ ID NO:2), as required by claim 8. Furthermore, with respect to the biological function of HSP91, the Examiner provides no evidence showing that HSP91 directly affects the formation or content of food storage reserves in *Arabidopsis*, much less any other plant. Given these differences, Storozhenko cannot anticipate the invention as presently claimed.

Finally, with respect to the rejection of claims 1-12 in view of Rounsley, applicants note that this reference is not prior art to the present claims. As evidence of this assertion, applicants direct the Examiner's attention to the attached Declaration of Dr. Yun Lin, where Dr. Lin attests to the fact that applicants identified and characterized the sequence encoding the Arabidopsis SSE prior to the February, 1999 publication date of Rounsley. Accordingly, the anticipation rejection in view of Rounsley can be withdrawn.

Rejections Under 35 U.S.C. § 103(a)

Claims 1, 3-7, 10-13, and 15-26 stand rejected under 35 U.S.C. 103(a) over Lee *et al.* (*supra*), in view of Dietrich *et al.* (Plant Physiol. 96:1268-1276, 1996) and Gordon-Kamm *et al.* (Plant Cell 2:603-618, 1990). Claims 1-13, 15-19, and 21-26 are rejected over Lee *et al.* (*supra*) in view of Storozhenko *et al.* (*supra*).

The invention covered by amended claims 1, 3-7, 10-13, and 15-22 is generally directed to isolated DNAs that encode SSE polypeptides having at least 30% identity to SEQ ID NO:2; vectors; cells; and plants including such DNAs. Claims 23-26 are generally directed to antisense SSE RNAs; vectors; cells; and plants expressing such antisense nucleic acids.

Applicants contend that none of the cited references, alone or in combination, discloses or suggests applicants' presently claimed nucleic acid compositions; cells; vectors; or plants and plant components. These references therefore cannot render the claimed invention obvious.

Looking first to the primary reference, Lee is cited as teaching the effects of transformation of *Arabidopsis* with an antisense HSP70 cDNA. Applicants note, however, neither the HSP70 nucleotide nor amino acid sequences meets the structural limitation of the claims. Alignment of either SEQ ID NO: 1 with accession number X63106 (cDNA encoding the HSP70 used by Lee) or SEQ ID NO: 2 with accession number CAA44820 (amino acid sequence encoded by X63106) demonstrates that the HSP70 of Lee is unrelated to the SSEs of the present invention. Moreover, the Office provides no evidence that HSP70 and SSE polypeptides are functionally interchangeable. Accordingly, Lee alone does not render the claimed SSE nucleic acids or polypeptides obvious.

Similarly, a conclusion that the claimed invention would have been obvious cannot be properly reached when either Lee is considered in view of Dietrich, Gordon-Kamm, or Storozhenko.

Dietrich, like Lee, teaches a heat shock protein from maize. Heat shock proteins are not SSE polypeptides. Dietrich and Lee in fact never suggest isolating plant DNA

molecules encoding SSE polypeptides, and never mention the idea that such SSE polypeptides exist. Dietrich and Lee therefore fail to teach any relevant details relating to the molecular biology or physiology of plant DNA molecules encoding a SSE polypeptide.

Gordon-Kamm discusses plant transformation and regeneration methods, but does not in any way teach or suggest isolating, expressing, or regulating a plant gene encoding an SSE polypeptide. The existence of the Gordon-Kamm reference that merely discloses how to transform and regenerate plants is insufficient, when combined with either Dietrich or Lee, to support a finding of obviousness.

In addition, as is discussed above, Storozhenko never suggests isolating DNA molecules encoding SSE polypeptides as presently claimed; and never mention the idea that antisense RNA could be used to modify plant storage reserves by regulating SSE gene expression. Storozhenko, like Lee, therefore fails to teach any relevant details relating to the molecular biology or physiology of DNA molecules encoding an SSE polypeptide having at least 30% identity to SEQ ID NO: 2, or hybridizing under stringency conditions to SEQ ID NO: 1, as presently claimed.

Applicants request reconsideration and withdrawal of these grounds of rejection.

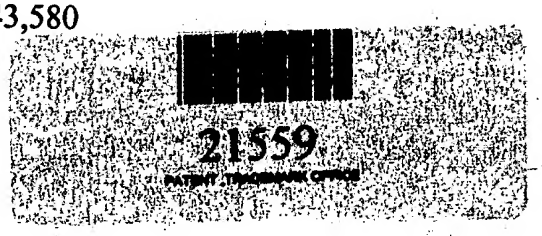
CONCLUSION

Applicants submit that the claims are in condition for allowance, and such action is requested. Enclosed is a petition to extend the period for replying for three months, to and including January 28, 2002, as January 27, 2002, falls on a Sunday. If there are any charges or any credits, please apply them to Deposit Account No. 03-2095.

Respectfully submitted,

Date: 28 January 2002

James D. DeCamp, Ph.D.
Reg. No. 43,580



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Version With Markings to Show Changes Made

In the Title:

[MODIFICATION OF PLANT STORAGE RESERVES] SSE NUCLEIC ACID MOLECULES AND USES THEREOF

In the Abstract:

Disclosed is a novel gene that is responsible for protein and oil body biogenesis. Methods and compositions are also provided for [producing plants exhibiting one or more desired phenotypic traits relating to] identifying genes having at least 30% identity to an Arabidopsis SSE1 polypeptide (SEQ ID NO:2). The invention further provides methods for using the disclosed genes for modifying the components of plant storage reserve materials.

In the Claims:

1. (Amended) An isolated nucleic acid molecule comprising a sequence encoding an SSE polypeptide having at least 30% identity with the amino acid sequence shown in Fig. 2B (SEQ ID NO: 2).

8. (Amended) An isolated nucleic acid molecule comprising a sequence encoding an SSE polypeptide, wherein said isolated nucleic acid molecule hybridizes [specifically] under low stringency conditions to the nucleic acid molecule comprising the cDNA of Fig. 2A (SEQ ID NO:1).

9. (Amended) The nucleic acid molecule of claim [1] 8, wherein said sequence encodes an SSE polypeptide having at least 30% identity with the amino acid sequence shown in Fig. 2B (SEQ ID NO:2).

12. (Amended) A cell [comprising] transformed with the isolated nucleic acid molecule of claim 1 or 8.

16. (Amended) A [transgenic] plant or [transgenic] plant component [comprising] transformed with a nucleic acid molecule of claim 1 or 8, wherein said nucleic acid molecule is expressed in said [transgenic] plant or said [transgenic] plant component.

Claims as Pending

1. (Amended) An isolated nucleic acid molecule comprising a sequence encoding an SSE polypeptide having at least 30% identity with the amino acid sequence shown in Fig. 2B (SEQ ID NO: 2).

3. The nucleic acid molecule of claim 1, wherein said sequence encodes an SSE polypeptide that, when expressed in a cell of a plant, modifies the production of food storage reserves.

4. The nucleic acid molecule of claim 1, wherein said sequence encodes an SSE polypeptide that, when expressed in a cell of a plant, facilitates the intracellular transport of a storage protein.

5. The nucleic acid molecule of claim 1, wherein said sequence encodes an SSE polypeptide that, when expressed in a cell of a plant, facilitates the formation of protein bodies.

6. The nucleic acid molecule of claim 1, wherein said sequence encodes an SSE polypeptide that, when expressed in a cell of a plant, facilitates the formation of oil bodies.

7. The nucleic acid molecule of claim 1, wherein said nucleic acid molecule is cDNA.

8. (Amended) An isolated nucleic acid molecule comprising a sequence encoding an SSE polypeptide, wherein said isolated nucleic acid molecule hybridizes under low stringency conditions to the nucleic acid molecule comprising the cDNA of Fig. 2A (SEQ ID NO:1).

9. (Amended) The nucleic acid molecule of claim 8, wherein said sequence encodes an SSE polypeptide having at least 30% identity with the amino acid sequence shown in Fig. 2B (SEQ ID NO:2).

10. The isolated nucleic acid molecule of claim 1 or 8, wherein said nucleic acid molecule is operably linked to a promoter functional in a plant cell.

11. An expression vector comprising the nucleic acid molecule of claim 1 or 8, said vector being capable of directing expression of the polypeptide encoded by said nucleic acid molecule.

12. (Amended) A cell transformed with the isolated nucleic acid molecule of claim 1 or 8.

13. The cell of claim 12, wherein said cell is a plant cell.

15. The cell of claim 12, wherein said bacterial cell is *Agrobacterium*.

16. (Amended) A plant or plant component transformed with a nucleic acid molecule of claim 1 or 8, wherein said nucleic acid molecule is expressed in said plant or said plant component.

17. The plant or plant component of claim 16, wherein said transgenic plant or transgenic plant component is an angiosperm.

18. The plant or plant component of claim 16, wherein said transgenic plant or transgenic plant component is a dicot.

19. The plant or plant component of claim 16, wherein said transgenic plant or transgenic plant component is a cruciferous plant.

20. The plant or plant component of claim 16, wherein said transgenic plant or transgenic plant component is a monocot.

21. A seed from a transgenic plant or transgenic plant component of claim 16.

22. A cell from a transgenic plant or transgenic plant component of claim 16.

23. An expression vector for producing antisense SSE RNA.

24. A transgenic plant or transgenic plant component comprising the vector of claim 23.

25. A seed from a transgenic plant or transgenic plant component of claim 24.

26. A cell from a transgenic plant or transgenic plant component of claim 24.